



## SEQUENCE LISTING

<110> Zankel et al.  
<120> MEGALIN-BASED DELIVERY OF THERAPEUTIC COMPOUNDS TO THE BRAIN AND OTHER TISSUES  
<130> 31075/40037  
<140> 10/812,849  
<141> 2004-03-30  
<150> US 10/600,862  
<151> 2003-06-20  
<160> 29  
<170> PatentIn version 3.2  
<210> 1  
<211> 323  
<212> PRT  
<213> Homo sapiens  
<400> 1

Tyr Ser Arg Glu Lys Asn Gln Pro Lys Pro Ser Pro Lys Arg Glu Ser  
1 5 10 15

Gly Glu Glu Phe Arg Met Glu Lys Leu Asn Gln Leu Trp Glu Lys Ala  
20 25 30

Gln Arg Leu His Leu Pro Pro Val Arg Leu Ala Glu Leu His Ala Asp  
35 40 45

Leu Lys Ile Gln Glu Arg Asp Glu Leu Ala Trp Lys Lys Leu Lys Leu  
50 55 60

Asp Gly Leu Asp Glu Asp Gly Glu Lys Glu Ala Arg Leu Ile Arg Asn  
65 70 75 80

Leu Asn Val Ile Leu Ala Lys Tyr Gly Leu Asp Gly Lys Lys Asp Ala  
85 90 95

Arg Gln Val Thr Ser Asn Ser Leu Ser Gly Thr Gln Glu Asp Gly Leu  
100 105 110

Asp Asp Pro Arg Leu Glu Lys Leu Trp His Lys Ala Lys Thr Ser Gly  
115 120 125

Lys Phe Ser Gly Glu Glu Leu Asp Lys Leu Trp Arg Glu Phe Leu His  
130 135 140

His Lys Glu Lys Val His Glu Tyr Asn Val Leu Leu Glu Thr Leu Ser  
145 150 155 160

Arg Thr Glu Glu Ile His Glu Asn Val Ile Ser Pro Ser Asp Leu Ser  
165 170 175

Asp Ile Lys Gly Ser Val Leu His Ser Arg His Thr Glu Leu Lys Glu  
180 185 190

Lys Leu Arg Ser Ile Asn Gln Gly Leu Asp Arg Leu Arg Arg Val Ser  
195 200 205

His Gln Gly Tyr Ser Thr Glu Ala Glu Phe Glu Glu Pro Arg Val Ile  
210 215 220

Asp Leu Trp Asp Leu Ala Gln Ser Ala Asn Leu Thr Asp Lys Glu Leu  
225 230 235 240

Glu Ala Phe Arg Glu Glu Leu Lys His Phe Glu Ala Lys Ile Glu Lys  
245 250 255

His Asn His Tyr Gln Lys Gln Leu Glu Ile Ala His Glu Lys Leu Arg  
260 265 270

His Ala Glu Ser Val Gly Asp Gly Glu Arg Val Ser Arg Ser Arg Glu  
275 280 285

Lys His Ala Leu Leu Glu Gly Arg Thr Lys Glu Leu Gly Tyr Thr Val  
290 295 300

Lys Lys His Leu Gln Asp Leu Ser Gly Arg Ile Ser Arg Ala Arg His  
305 310 315 320

Asn Glu Leu

<210> 2  
<211> 209  
<212> PRT  
<213> Homo sapiens

<400> 2

Pro Arg Leu Glu Lys Leu Trp His Lys Ala Lys Thr Ser Gly Lys Phe  
1 5 10 15

Ser Gly Glu Glu Leu Asp Lys Leu Trp Arg Glu Phe Leu His His Lys  
20 25 30

Glu Lys Val His Glu Tyr Asn Val Leu Leu Glu Thr Leu Ser Arg Thr

35	40	45	
Glu Glu Ile His Glu Asn Val Ile Ser Pro Ser Asp Leu Ser Asp Ile			
50	55	60	
Lys Gly Ser Val Leu His Ser Arg His Thr Glu Leu Lys Glu Lys Leu			
65	70	75	80
Arg Ser Ile Asn Gln Gly Leu Asp Arg Leu Arg Arg Val Ser His Gln			
	85	90	95
Gly Tyr Ser Thr Glu Ala Glu Phe Glu Glu Pro Arg Val Ile Asp Leu			
	100	105	110
Trp Asp Leu Ala Gln Ser Ala Asn Leu Thr Asp Lys Glu Leu Glu Ala			
	115	120	125
Phe Arg Glu Glu Leu Lys His Phe Glu Ala Lys Ile Glu Lys His Asn			
	130	135	140
His Tyr Gln Lys Gln Leu Glu Ile Ala His Glu Lys Leu Arg His Ala			
	145	150	155
Glu Ser Val Gly Asp Gly Glu Arg Val Ser Arg Ser Arg Glu Lys His			
	165	170	175
Ala Leu Leu Glu Gly Arg Thr Lys Glu Leu Gly Tyr Thr Val Lys Lys			
	180	185	190
His Leu Gln Asp Leu Ser Gly Arg Ile Ser Arg Ala Arg His Asn Glu			
	195	200	205
Leu			

<210> 3  
 <211> 33  
 <212> DNA  
 <213> Artificial sequence  
  
 <220>  
 <223> Synthetic primer  
  
 <400> 3  
 ccgcgtggat cccccaggct ggaaaagctg tgg

33

<210> 4  
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 <212> DNA  
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<220>  
 <223> Synthetic primer  
 <400> 4  
 tcaatgaatt ctcagagttc gttgtgccga gctct

35

<210> 5  
 <211> 205  
 <212> PRT  
 <213> Homo sapiens

<400> 5

Pro Arg Leu Glu Lys Leu Trp His Lys Ala Lys Thr Ser Gly Ile Ser  
 1 5 10 15

Val Arg Leu Thr Ser Cys Ala Arg Val Leu His Tyr Lys Glu Lys Ile  
 20 25 30

His Glu Tyr Asn Val Leu Leu Asp Thr Leu Ser Arg Ala Glu Glu Gly  
 35 40 45

Tyr Glu Asn Leu Leu Ser Pro Ser Asp Met Thr His Ile Lys Ser Asp  
 50 55 60

Thr Leu Ala Ser Lys His Ser Glu Leu Lys Asp Arg Leu Arg Ser Ile  
 65 70 75 80

Asn Gln Gly Leu Asp Arg Leu Arg Lys Val Ser His Gln Leu Arg Pro  
 85 90 95

Ala Thr Glu Phe Glu Glu Pro Arg Val Ile Asp Leu Trp Asp Leu Ala  
 100 105 110

Gln Ser Ala Asn Phe Thr Glu Lys Glu Leu Glu Ser Phe Arg Glu Glu  
 115 120 125

Leu Lys His Phe Glu Ala Lys Ile Glu Lys His Asn His Tyr Gln Lys  
 130 135 140

Gln Leu Glu Ile Ser His Gln Lys Leu Lys His Val Glu Ser Ile Gly  
 145 150 155 160

Asp Pro Glu His Ile Ser Arg Asn Lys Glu Lys Tyr Val Leu Leu Glu  
 165 170 175

Glu Lys Thr Lys Glu Leu Gly Tyr Lys Val Lys Lys His Leu Gln Asp  
 180 185 190

Leu Ser Ser Arg Val Ser Arg Ala Arg His Asn Glu Leu

<210> 6  
 <211> 3702  
 <212> DNA  
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<220>  
 <223> RAP-GAA fusion sequence

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 gaggagtcc gcattggagaa gttgaaccag ctgtgggaga aggcccagcg actgcatctt 180  
 cctcccgtga ggctggccga gctccacgt gatctgaaga tacaggagag ggacgaactc 240  
 gcctggaaga aactaaagct tgacggcttg gacgaagatg gggagaagga agcgagactc 300  
 atacgcaacc tcaatgtcat cttggccaag tatgggtctgg acggaaagaa ggacgctcgg 360  
 caggtgacca gcaactccct cagtggcacc caggaagacg ggctggatga cccagggctg 420  
 gaaaagctgt ggcacaaggc gaagacctct gggaaattct ccggcgaaga actggacaag 480  
 ctctggcggg agttcctgca tcacaaagag aaagttcacg agtacaacgt cctgctggag 540  
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 atcaagggca gcgtcctgca cagcaggcac acggagctga aggagaagct gcgcagcatc 660  
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 ttcgaggagc ccagggtgat tgacctgtgg gacctggcgc agtccgcca cctcacggac 780  
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 ggcgacggcg agcgtgtgag ccgcagccgc gagaagcacg ccctgctgga ggggcggacc 960  
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 gctcgcgccg aggcagaaac cgggtgcacac cccggccgtc ccagagcagt gcccacacag 1080  
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accgtggccc	ggccccctct	cctggagttc	ccaaggact	ctagcacctg	gactgtggac	3060
caccagctcc	tgtgggggga	ggccttgctc	atcaccccag	tgtccaggc	cgggaaggcc	3120
gaagtgactg	gctacttccc	cttgggcaca	tggtacgacc	tgcagacggt	gccaatagag	3180
gcccttggca	gcctcccacc	cccacctgca	gctccccgtg	agccagccat	ccacagcgag	3240
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tacatcatcc	ccctgcaggg	ccctggcctc	acaaccacag	agtcccgcga	gcagcccatg	3360
gccctggctg	tggccctaac	caaggggtga	gaggcccgag	gggagctgtt	ctgggacgat	3420
ggagagagcc	tggaagtgct	ggagcgaggg	gcctacacac	aggtcatctt	cctggccagg	3480

aataacacga tcgtgaatga gctggtacgt gtgaccagtg agggagctgg cctgcagctg 3540  
 cagaaggtga ctgtcctggg cgtggccacg gcgccccagc aggtcctctc caacgggtgc 3600  
 cctgtctcca acttcaccta cagccccgac accaaggtcc tggacatctg tgtctcgctg 3660  
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<210> 7  
 <211> 1228  
 <212> PRT  
 <213> Artificial sequence  
 <220>  
 <223> RAP-GAA fusion sequence  
 <400> 7

Met Arg Gly Pro Ser Gly Ala Leu Trp Leu Leu Leu Ala Leu Arg Thr  
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Val Leu Gly Ser Tyr Ser Arg Glu Lys Asn Gln Pro Lys Pro Ser Pro  
 20 25 30

Lys Arg Glu Ser Gly Glu Glu Phe Arg Met Glu Lys Leu Asn Gln Leu  
 35 40 45

Trp Glu Lys Ala Gln Arg Leu His Leu Pro Pro Val Arg Leu Ala Glu  
 50 55 60

Leu His Ala Asp Leu Lys Ile Gln Glu Arg Asp Glu Leu Ala Trp Lys  
 65 70 75 80

Lys Leu Lys Leu Asp Gly Leu Asp Glu Asp Gly Glu Lys Glu Ala Arg  
 85 90 95

Leu Ile Arg Asn Leu Asn Val Ile Leu Ala Lys Tyr Gly Leu Asp Gly  
 100 105 110

Lys Lys Asp Ala Arg Gln Val Thr Ser Asn Ser Leu Ser Gly Thr Gln  
 115 120 125

Glu Asp Gly Leu Asp Asp Pro Arg Leu Glu Lys Leu Trp His Lys Ala  
 130 135 140

Lys Thr Ser Gly Lys Phe Ser Gly Glu Glu Leu Asp Lys Leu Trp Arg  
 145 150 155 160

Glu Phe Leu His His Lys Glu Lys Val His Glu Tyr Asn Val Leu Leu  
 165 170 175

Glu Thr Leu Ser Arg Thr Glu Glu Ile His Glu Asn Val Ile Ser Pro  
 180 185 190  
 Ser Asp Leu Ser Asp Ile Lys Gly Ser Val Leu His Ser Arg His Thr  
 195 200 205  
 Glu Leu Lys Glu Lys Leu Arg Ser Ile Asn Gln Gly Leu Asp Arg Leu  
 210 215 220  
 Arg Arg Val Ser His Gln Gly Tyr Ser Thr Glu Ala Glu Phe Glu Glu  
 225 230 235 240  
 Pro Arg Val Ile Asp Leu Trp Asp Leu Ala Gln Ser Ala Asn Leu Thr  
 245 250 255  
 Asp Lys Glu Leu Glu Ala Phe Arg Glu Glu Leu Lys His Phe Glu Ala  
 260 265 270  
 Lys Ile Glu Lys His Asn His Tyr Gln Lys Gln Leu Glu Ile Ala His  
 275 280 285  
 Glu Lys Leu Arg His Ala Glu Ser Val Gly Asp Gly Glu Arg Val Ser  
 290 295 300  
 Arg Ser Arg Glu Lys His Ala Leu Leu Glu Gly Arg Thr Lys Glu Leu  
 305 310 315 320  
 Gly Tyr Thr Val Lys Lys His Leu Gln Asp Leu Ser Gly Arg Ile Ser  
 325 330 335  
 Arg Ala Arg Ala Glu Ala Glu Thr Gly Ala His Pro Gly Arg Pro Arg  
 340 345 350  
 Ala Val Pro Thr Gln Cys Asp Val Pro Pro Asn Ser Arg Phe Asp Cys  
 355 360 365  
 Ala Pro Asp Lys Ala Ile Thr Gln Glu Gln Cys Glu Ala Arg Gly Cys  
 370 375 380  
 Cys Tyr Ile Pro Ala Lys Gln Gly Leu Gln Gly Ala Gln Met Gly Gln  
 385 390 395 400  
 Pro Trp Cys Phe Phe Pro Pro Ser Tyr Pro Ser Tyr Lys Leu Glu Asn  
 405 410 415  
 Leu Ser Ser Ser Glu Met Gly Tyr Thr Ala Thr Leu Thr Arg Thr Thr  
 420 425 430



Pro Thr Phe Phe Pro Lys Asp Ile Leu Thr Leu Arg Leu Asp Val Met  
 435 440 445

Met Glu Thr Glu Asn Arg Leu His Phe Thr Ile Lys Asp Pro Ala Asn  
 450 455 460

Arg Arg Tyr Glu Val Pro Leu Glu Thr Pro Arg Val His Ser Arg Ala  
 465 470 475 480

Pro Ser Pro Leu Tyr Ser Val Glu Phe Ser Glu Glu Pro Phe Gly Val  
 485 490 495

Ile Val His Arg Gln Leu Asp Gly Arg Val Leu Leu Asn Thr Thr Val  
 500 505 510

Ala Pro Leu Phe Phe Ala Asp Gln Phe Leu Gln Leu Ser Thr Ser Leu  
 515 520 525

Pro Ser Gln Tyr Ile Thr Gly Leu Ala Glu His Leu Ser Pro Leu Met  
 530 535 540

Leu Ser Thr Ser Trp Thr Arg Ile Thr Leu Trp Asn Arg Asp Leu Ala  
 545 550 555 560

Pro Thr Pro Gly Ala Asn Leu Tyr Gly Ser His Pro Phe Tyr Leu Ala  
 565 570 575

Leu Glu Asp Gly Gly Ser Ala His Gly Val Phe Leu Leu Asn Ser Asn  
 580 585 590

Ala Met Asp Val Val Leu Gln Pro Ser Pro Ala Leu Ser Trp Arg Ser  
 595 600 605

Thr Gly Gly Ile Leu Asp Val Tyr Ile Phe Leu Gly Pro Glu Pro Lys  
 610 615 620

Ser Val Val Gln Gln Tyr Leu Asp Val Val Gly Tyr Pro Phe Met Pro  
 625 630 635 640

Pro Tyr Trp Gly Leu Gly Phe His Leu Cys Arg Trp Gly Tyr Ser Ser  
 645 650 655

Thr Ala Ile Thr Arg Gln Val Val Glu Asn Met Thr Arg Ala His Phe  
 660 665 670

Pro Leu Asp Val Gln Trp Asn Asp Leu Asp Tyr Met Asp Ser Arg Arg  
 675 680 685

Asp Phe Thr Phe Asn Lys Asp Gly Phe Arg Asp Phe Pro Ala Met Val  
 690 695 700

Gln Glu Leu His Gln Gly Gly Arg Arg Tyr Met Met Ile Val Asp Pro  
 705 710 715 720

Ala Ile Ser Ser Ser Gly Pro Ala Gly Ser Tyr Arg Pro Tyr Asp Glu  
 725 730 735

Gly Leu Arg Arg Gly Val Phe Ile Thr Asn Glu Thr Gly Gln Pro Leu  
 740 745 750

Ile Gly Lys Val Trp Pro Gly Ser Thr Ala Phe Pro Asp Phe Thr Asn  
 755 760 765

Pro Thr Ala Leu Ala Trp Trp Glu Asp Met Val Ala Glu Phe His Asp  
 770 775 780

Gln Val Pro Phe Asp Gly Leu Trp Ile Asp Met Asn Glu Pro Ser Asn  
 785 790 795 800

Phe Ile Arg Gly Ser Glu Asp Gly Cys Pro Asn Asn Glu Leu Glu Asn  
 805 810 815

Pro Pro Tyr Val Pro Gly Val Val Gly Gly Thr Leu Gln Ala Ala Thr  
 820 825 830

Ile Cys Ala Ser Ser His Gln Phe Leu Ser Thr His Tyr Asn Leu His  
 835 840 845

Asn Leu Tyr Gly Leu Thr Glu Ala Ile Ala Ser His Arg Ala Leu Val  
 850 855 860

Lys Ala Arg Gly Thr Arg Pro Phe Val Ile Ser Arg Ser Thr Phe Ala  
 865 870 875 880

Gly His Gly Arg Tyr Ala Gly His Trp Thr Gly Asp Val Trp Ser Ser  
 885 890 895

Trp Glu Gln Leu Ala Ser Ser Val Pro Glu Ile Leu Gln Phe Asn Leu  
 900 905 910

Leu Gly Val Pro Leu Val Gly Ala Asp Val Cys Gly Phe Leu Gly Asn  
 915 920 925

Thr Ser Glu Glu Leu Cys Val Arg Trp Thr Gln Leu Gly Ala Phe Tyr  
 930 935 940

Pro Phe Met Arg Asn His Asn Ser Leu Leu Ser Leu Pro Gln Glu Pro  
 945 950 955 960

Tyr Ser Phe Ser Glu Pro Ala Gln Gln Ala Met Arg Lys Ala Leu Thr  
 965 970 975

Leu Arg Tyr Ala Leu Leu Pro His Leu Tyr Thr Leu Phe His Gln Ala  
 980 985 990

His Val Ala Gly Glu Thr Val Ala Arg Pro Leu Phe Leu Glu Phe Pro  
 995 1000 1005

Lys Asp Ser Ser Thr Trp Thr Val Asp His Gln Leu Leu Trp Gly  
 1010 1015 1020

Glu Ala Leu Leu Ile Thr Pro Val Leu Gln Ala Gly Lys Ala Glu  
 1025 1030 1035

Val Thr Gly Tyr Phe Pro Leu Gly Thr Trp Tyr Asp Leu Gln Thr  
 1040 1045 1050

Val Pro Ile Glu Ala Leu Gly Ser Leu Pro Pro Pro Pro Ala Ala  
 1055 1060 1065

Pro Arg Glu Pro Ala Ile His Ser Glu Gly Gln Trp Val Thr Leu  
 1070 1075 1080

Pro Ala Pro Leu Asp Thr Ile Asn Val His Leu Arg Ala Gly Tyr  
 1085 1090 1095

Ile Ile Pro Leu Gln Gly Pro Gly Leu Thr Thr Thr Glu Ser Arg  
 1100 1105 1110

Gln Gln Pro Met Ala Leu Ala Val Ala Leu Thr Lys Gly Gly Glu  
 1115 1120 1125

Ala Arg Gly Glu Leu Phe Trp Asp Asp Gly Glu Ser Leu Glu Val  
 1130 1135 1140

Leu Glu Arg Gly Ala Tyr Thr Gln Val Ile Phe Leu Ala Arg Asn  
 1145 1150 1155

Asn Thr Ile Val Asn Glu Leu Val Arg Val Thr Ser Glu Gly Ala  
 1160 1165 1170

Gly Leu Gln Leu Gln Lys Val Thr Val Leu Gly Val Ala Thr Ala  
 1175 1180 1185

Pro Gln Gln Val Leu Ser Asn Gly Val Pro Val Ser Asn Phe Thr  
 1190 1195 1200

Tyr Ser Pro Asp Thr Lys Val Leu Asp Ile Cys Val Ser Leu Leu  
 1205 1210 1215

Met Gly Glu Gln Phe Leu Val Ser Trp Cys  
 1220 1225

<210> 8  
 <211> 2937  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <223> RAP-IDU fusion sequence

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gtgggcgtcc	tggccagcgc	ccaccgcccc	cagggcccgg	ccgacgcctg	gcgcgcgcgcg	2280
gtgctgatct	acgcgagcga	cgacaccgcg	gcccacccca	accgcagcgt	cgcggtgacc	2340
ctgcggctgc	gcgggggtgcc	ccccggcccc	ggcctgggtct	acgtcacgcg	ctacctggac	2400
aacgggctct	gcagccccga	cggcgagtgg	cggcgcctgg	gccggcccgt	cttccccacg	2460
gcagagcagt	tccggcgcat	gcgcgcgggt	gaggaccggg	tggccgcggc	gccccgcccc	2520
ttaccgcgg	gcggccgcct	gaccctgcgc	cccgcgctgc	ggctgccgtc	gcttttgctg	2580
gtgcacgtgt	gtgcgcgccc	cgagaagccg	cccgggcagg	tcacgcgggt	ccgcgcctctg	2640
cccctgaccc	aagggcagct	ggttctggtc	tggtcggatg	aacacgtggg	ctccaagtgc	2700
ctgtggacat	acgagatcca	gttctctcag	gacggtaagg	cgtacacccc	ggtcagcagg	2760
aagccatcga	ccttcaacct	ctttgtgttc	agcccagaca	caggtgctgt	ctctggctcc	2820
taccgagttc	gagccctgga	ctactgggcc	cgaccaggcc	ccttctcgga	ccctgtgccg	2880
tacctggagg	tccctgtgcc	aagagggccc	ccatccccgg	gcaatccatg	actcgag	2937

<210> 9  
 <211> 972  
 <212> PRT  
 <213> Artificial sequence  
 <220>

<223> RAP-IDU fusion sequence

<400> 9

Met Arg Gly Pro Ser Gly Ala Leu Trp Leu Leu Leu Ala Leu Arg Thr  
1 5 10 15

Val Leu Gly Ser Tyr Ser Arg Glu Lys Asn Gln Pro Lys Pro Ser Pro  
20 25 30

Lys Arg Glu Ser Gly Glu Glu Phe Arg Met Glu Lys Leu Asn Gln Leu  
35 40 45

Trp Glu Lys Ala Gln Arg Leu His Leu Pro Pro Val Arg Leu Ala Glu  
50 55 60

Leu His Ala Asp Leu Lys Ile Gln Glu Arg Asp Glu Leu Ala Trp Lys  
65 70 75 80

Lys Leu Lys Leu Asp Gly Leu Asp Glu Asp Gly Glu Lys Glu Ala Arg  
85 90 95

Leu Ile Arg Asn Leu Asn Val Ile Leu Ala Lys Tyr Gly Leu Asp Gly  
100 105 110

Lys Lys Asp Ala Arg Gln Val Thr Ser Asn Ser Leu Ser Gly Thr Gln  
115 120 125

Glu Asp Gly Leu Asp Asp Pro Arg Leu Glu Lys Leu Trp His Lys Ala  
130 135 140

Lys Thr Ser Gly Lys Phe Ser Gly Glu Glu Leu Asp Lys Leu Trp Arg  
145 150 155 160

Glu Phe Leu His His Lys Glu Lys Val His Glu Tyr Asn Val Leu Leu  
165 170 175

Glu Thr Leu Ser Arg Thr Glu Glu Ile His Glu Asn Val Ile Ser Pro  
180 185 190

Ser Asp Leu Ser Asp Ile Lys Gly Ser Val Leu His Ser Arg His Thr  
195 200 205

Glu Leu Lys Glu Lys Leu Arg Ser Ile Asn Gln Gly Leu Asp Arg Leu  
210 215 220

Arg Arg Val Ser His Gln Gly Tyr Ser Thr Glu Ala Glu Phe Glu Glu  
225 230 235 240

Pro Arg Val Ile Asp Leu Trp Asp Leu Ala Gln Ser Ala Asn Leu Thr  
                   245                                  250                                  255

Asp Lys Glu Leu Glu Ala Phe Arg Glu Glu Leu Lys His Phe Glu Ala  
                   260                                  265                                  270

Lys Ile Glu Lys His Asn His Tyr Gln Lys Gln Leu Glu Ile Ala His  
                   275                                  280                                  285

Glu Lys Leu Arg His Ala Glu Ser Val Gly Asp Gly Glu Arg Val Ser  
                   290                                  295                                  300

Arg Ser Arg Glu Lys His Ala Leu Leu Glu Gly Arg Thr Lys Glu Leu  
                   305                                  310                                  315                                  320

Gly Tyr Thr Val Lys Lys His Leu Gln Asp Leu Ser Gly Arg Ile Ser  
                                   325                                  330                                  335

Arg Ala Arg Ala Glu Ala Glu Thr Gly Glu Ala Pro His Leu Val His  
                                   340                                  345                                  350

Val Asp Ala Ala Arg Ala Leu Trp Pro Leu Arg Arg Phe Trp Arg Ser  
                   355                                  360                                  365

Thr Gly Phe Cys Pro Pro Leu Pro His Ser Gln Ala Asp Gln Tyr Val  
                   370                                  375                                  380

Leu Ser Trp Asp Gln Gln Leu Asn Leu Ala Tyr Val Gly Ala Val Pro  
                   385                                  390                                  395                                  400

His Arg Gly Ile Lys Gln Val Arg Thr His Trp Leu Leu Glu Leu Val  
                                   405                                  410                                  415

Thr Thr Arg Gly Ser Thr Gly Arg Gly Leu Ser Tyr Asn Phe Thr His  
                                   420                                  425                                  430

Leu Asp Gly Tyr Leu Asp Leu Leu Arg Glu Asn Gln Leu Leu Pro Gly  
                   435                                  440                                  445

Phe Glu Leu Met Gly Ser Ala Ser Gly His Phe Thr Asp Phe Glu Asp  
                   450                                  455                                  460

Lys Gln Gln Val Phe Glu Trp Lys Asp Leu Val Ser Ser Leu Ala Arg  
                   465                                  470                                  475                                  480

Arg Tyr Ile Gly Arg Tyr Gly Leu Ala His Val Ser Lys Trp Asn Phe  
                                   485                                  490                                  495

Glu Thr Trp Asn Glu Pro Asp His His Asp Phe Asp Asn Val Ser Met  
 500 505 510

Thr Met Gln Gly Phe Leu Asn Tyr Tyr Asp Ala Cys Ser Glu Gly Leu  
 515 520 525

Arg Ala Ala Ser Pro Ala Leu Arg Leu Gly Gly Pro Gly Asp Ser Phe  
 530 535 540

His Thr Pro Pro Arg Ser Pro Leu Ser Trp Gly Leu Leu Arg His Cys  
 545 550 555 560

His Asp Gly Thr Asn Phe Phe Thr Gly Glu Ala Gly Val Arg Leu Asp  
 565 570 575

Tyr Ile Ser Leu His Arg Lys Gly Ala Arg Ser Ser Ile Ser Ile Leu  
 580 585 590

Glu Gln Glu Lys Val Val Ala Gln Gln Ile Arg Gln Leu Phe Pro Lys  
 595 600 605

Phe Ala Asp Thr Pro Ile Tyr Asn Asp Glu Ala Asp Pro Leu Val Gly  
 610 615 620

Trp Ser Leu Pro Gln Pro Trp Arg Ala Asp Val Thr Tyr Ala Ala Met  
 625 630 635 640

Val Val Lys Val Ile Ala Gln His Gln Asn Leu Leu Leu Ala Asn Thr  
 645 650 655

Thr Ser Ala Phe Pro Tyr Ala Leu Leu Ser Asn Asp Asn Ala Phe Leu  
 660 665 670

Ser Tyr His Pro His Pro Phe Ala Gln Arg Thr Leu Thr Ala Arg Phe  
 675 680 685

Gln Val Asn Asn Thr Arg Pro Pro His Val Gln Leu Leu Arg Lys Pro  
 690 695 700

Val Leu Thr Ala Met Gly Leu Leu Ala Leu Leu Asp Glu Glu Gln Leu  
 705 710 715 720

Trp Ala Glu Val Ser Gln Ala Gly Thr Val Leu Asp Ser Asn His Thr  
 725 730 735

Val Gly Val Leu Ala Ser Ala His Arg Pro Gln Gly Pro Ala Asp Ala  
 740 745 750



Trp Arg Ala Ala Val Leu Ile Tyr Ala Ser Asp Asp Thr Arg Ala His  
755 760 765

Pro Asn Arg Ser Val Ala Val Thr Leu Arg Leu Arg Gly Val Pro Pro  
770 775 780

Gly Pro Gly Leu Val Tyr Val Thr Arg Tyr Leu Asp Asn Gly Leu Cys  
785 790 795 800

Ser Pro Asp Gly Glu Trp Arg Arg Leu Gly Arg Pro Val Phe Pro Thr  
805 810 815

Ala Glu Gln Phe Arg Arg Met Arg Ala Ala Glu Asp Pro Val Ala Ala  
820 825 830

Ala Pro Arg Pro Leu Pro Ala Gly Gly Arg Leu Thr Leu Arg Pro Ala  
835 840 845

Leu Arg Leu Pro Ser Leu Leu Leu Val His Val Cys Ala Arg Pro Glu  
850 855 860

Lys Pro Pro Gly Gln Val Thr Arg Leu Arg Ala Leu Pro Leu Thr Gln  
865 870 875 880

Gly Gln Leu Val Leu Val Trp Ser Asp Glu His Val Gly Ser Lys Cys  
885 890 895

Leu Trp Thr Tyr Glu Ile Gln Phe Ser Gln Asp Gly Lys Ala Tyr Thr  
900 905 910

Pro Val Ser Arg Lys Pro Ser Thr Phe Asn Leu Phe Val Phe Ser Pro  
915 920 925

Asp Thr Gly Ala Val Ser Gly Ser Tyr Arg Val Arg Ala Leu Asp Tyr  
930 935 940

Trp Ala Arg Pro Gly Pro Phe Ser Asp Pro Val Pro Tyr Leu Glu Val  
945 950 955 960

Pro Val Pro Arg Gly Pro Pro Ser Pro Gly Asn Pro  
965 970

<210> 10

<211> 1398

<212> DNA

<213> Artificial sequence

<220>

<223> RAP-GDNF fusion sequence

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<400> 10
atgggggggtt cttactcgcg ggagaagaac cagcccgaagc cgtccccgaa acgcgagtc 60
ggagaggagt tccgcatgga gaagttgaac cagctgtggg agaaggcca gcgactgcat 120
cttcctcccg tgaggctggc cgagctccac gctgatctga agatacagga gagggacgaa 180
ctcgcttggga agaaactaaa gcttgacggc ttggacgaag atggggagaa ggaagcgaga 240
ctcatacgca acctcaatgt catcttggcc aagtatggtc tggacggaaa gaaggacgct 300
cggcaggtga ccagcaactc cctcagtggc acccaggaag acgggctgga tgaccccagg 360
ctggaaaagc tgtggcaca ggcaagacc tctgggaaat tctccggcga agaactggac 420
aagctctggc gggagttcct gcatcacaaa gagaaagttc acgagtacaa cgtcctgctg 480
gagaccctga gcaggaccga agaaatccac gagaacgtca ttagcccctc ggacctgagc 540
gacatcaagg gcagcgtcct gcacagcagg cacacggagc tgaaggagaa gctgcgagc 600
atcaaccagg gcctggaccg cctgcgagc gtcagccacc agggctacag cactgaggct 660
gagttcgagg agcccagggt gattgacctg tgggacctgg cgcagtccgc caacctcacg 720
gacaaggagc tggaggcggt ccgggaggag ctcaagcact tcgaagccaa aatcgagaag 780
cacaaccact accagaagca gctggagatt gcgcacgaga agctgaggca cgcagagagc 840
gtgggcgacg gcgagcgtgt gagccgcagc cgcgagaagc acgccctgct ggaggggagg 900
accaaggagc tgggctacac ggtgaagaag catctgcagg acctgtccgg caggatctcc 960
agagctcggg ccgaggcaga aaccggttca ccagataaac aaatggcagt gcttcctaga 1020
agagagcggg atcggcaggc tgcagctgcc aaccagaga attccagagg aaaaggctcg 1080
agaggccaga ggggcaaaaa ccgggggtgt gtcttaactg caatacattt aaatgtcact 1140
gacttgggtc tgggctatga aaccaaggag gaactgattt ttaggtactg cagcggctct 1200
tgcgatgcag ctgagacaac gtacgacaaa atattgaaaa acttatccag aaatagaagg 1260
ctggtgagtg acaaagtagg gcaggcatgt tgcagacca tcgcctttga tgatgacctg 1320
tcgttttttag atgataacct ggtttaccat attctaagaa agcattccgc taaaagggtg 1380
ggatgtatct gatctaga 1398

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<210> 11
<211> 463
<212> PRT
<213> Artificial sequence

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<220>
<223> RAP-GDNF fusion sequence

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<400> 11

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Met Gly Gly Ser Tyr Ser Arg Glu Lys Asn Gln Pro Lys Pro Ser Pro
1           5           10           15

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Lys Arg Glu Ser Gly Glu Glu Phe Arg Met Glu Lys Leu Asn Gln Leu  
 20 25 30

Trp Glu Lys Ala Gln Arg Leu His Leu Pro Pro Val Arg Leu Ala Glu  
 35 40 45

Leu His Ala Asp Leu Lys Ile Gln Glu Arg Asp Glu Leu Ala Trp Lys  
 50 55 60

Lys Leu Lys Leu Asp Gly Leu Asp Glu Asp Gly Glu Lys Glu Ala Arg  
 65 70 75 80

Leu Ile Arg Asn Leu Asn Val Ile Leu Ala Lys Tyr Gly Leu Asp Gly  
 85 90 95

Lys Lys Asp Ala Arg Gln Val Thr Ser Asn Ser Leu Ser Gly Thr Gln  
 100 105 110

Glu Asp Gly Leu Asp Asp Pro Arg Leu Glu Lys Leu Trp His Lys Ala  
 115 120 125

Lys Thr Ser Gly Lys Phe Ser Gly Glu Glu Leu Asp Lys Leu Trp Arg  
 130 135 140

Glu Phe Leu His His Lys Glu Lys Val His Glu Tyr Asn Val Leu Leu  
 145 150 155 160

Glu Thr Leu Ser Arg Thr Glu Glu Ile His Glu Asn Val Ile Ser Pro  
 165 170 175

Ser Asp Leu Ser Asp Ile Lys Gly Ser Val Leu His Ser Arg His Thr  
 180 185 190

Glu Leu Lys Glu Lys Leu Arg Ser Ile Asn Gln Gly Leu Asp Arg Leu  
 195 200 205

Arg Arg Val Ser His Gln Gly Tyr Ser Thr Glu Ala Glu Phe Glu Glu  
 210 215 220

Pro Arg Val Ile Asp Leu Trp Asp Leu Ala Gln Ser Ala Asn Leu Thr  
 225 230 235 240

Asp Lys Glu Leu Glu Ala Phe Arg Glu Glu Leu Lys His Phe Glu Ala  
 245 250 255

Lys Ile Glu Lys His Asn His Tyr Gln Lys Gln Leu Glu Ile Ala His  
 260 265 270

Glu Lys Leu Arg His Ala Glu Ser Val Gly Asp Gly Glu Arg Val Ser  
275 280 285

Arg Ser Arg Glu Lys His Ala Leu Leu Glu Gly Arg Thr Lys Glu Leu  
290 295 300

Gly Tyr Thr Val Lys Lys His Leu Gln Asp Leu Ser Gly Arg Ile Ser  
305 310 315 320

Arg Ala Arg Ala Glu Ala Glu Thr Gly Ser Pro Asp Lys Gln Met Ala  
325 330 335

Val Leu Pro Arg Arg Glu Arg Asn Arg Gln Ala Ala Ala Asn Pro  
340 345 350

Glu Asn Ser Arg Gly Lys Gly Arg Arg Gly Gln Arg Gly Lys Asn Arg  
355 360 365

Gly Cys Val Leu Thr Ala Ile His Leu Asn Val Thr Asp Leu Gly Leu  
370 375 380

Gly Tyr Glu Thr Lys Glu Glu Leu Ile Phe Arg Tyr Cys Ser Gly Ser  
385 390 395 400

Cys Asp Ala Ala Glu Thr Thr Tyr Asp Lys Ile Leu Lys Asn Leu Ser  
405 410 415

Arg Asn Arg Arg Leu Val Ser Asp Lys Val Gly Gln Ala Cys Cys Arg  
420 425 430

Pro Ile Ala Phe Asp Asp Asp Leu Ser Phe Leu Asp Asp Asn Leu Val  
435 440 445

Tyr His Ile Leu Arg Lys His Ser Ala Lys Arg Cys Gly Cys Ile  
450 455 460

<210> 12  
<211> 49  
<212> DNA  
<213> Artificial sequence

<220>  
<223> Synthetic primer

<400> 12  
gcgataggat cctactcgcg ggagaagaac cagcccaagc cgtccccga

49

<210> 13  
<211> 57  
<212> DNA

<213> Artificial sequence  
 <220>  
 <223> Synthetic primer  
 <400> 13  
 gcgataaacc ggtttctgcc tcggcgcgag ctctggagat cctgccggac aggtcct 57  
 <210> 14  
 <211> 39  
 <212> DNA  
 <213> Artificial sequence  
 <220>  
 <223> Synthetic primer  
 <400> 14  
 gcgataaccg gtgcacaccc cggccgtccc agagcagtg 39  
 <210> 15  
 <211> 37  
 <212> DNA  
 <213> Artificial sequence  
 <220>  
 <223> Synthetic primer  
 <400> 15  
 gcgatactcg agtcaacacc agctgacgag aaactgc 37  
 <210> 16  
 <211> 46  
 <212> DNA  
 <213> Artificial sequence  
 <220>  
 <223> Synthetic primer  
 <400> 16  
 gcgataaccg gtgaggcccc ccgcacctgg tgcattgtgga cgcggc 46  
 <210> 17  
 <211> 45  
 <212> DNA  
 <213> Artificial sequence  
 <220>  
 <223> Synthetic primer  
 <400> 17  
 gcgatactcg agtcatggat tgcccgggga tgggggacct cttgg 45  
 <210> 18  
 <211> 33  
 <212> DNA  
 <213> Artificial sequence  
 <220>

<223> Synthetic primer

<400> 18

acagtgaccg gttcaccaga taaacaaatg gca

33

<210> 19

<211> 38

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic primer

<400> 19

acagtgctcg agtctagatc agatacatcc acaccttt

38

<210> 20

<211> 51

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic primer

<400> 20

acagtggcca tgggggggttc ttactcgcgg gagaagaacc agcccaagcc g

51

<210> 21

<211> 357

<212> PRT

<213> Homo sapiens

<400> 21

Met Ala Pro Arg Arg Val Arg Ser Phe Leu Arg Gly Leu Pro Ala Leu  
1 5 10 15

Leu Leu Leu Leu Leu Phe Leu Gly Pro Trp Pro Ala Ala Ser His Gly  
20 25 30

Gly Lys Tyr Ser Arg Glu Lys Asn Gln Pro Lys Pro Ser Pro Lys Arg  
35 40 45

Glu Ser Gly Glu Glu Phe Arg Met Glu Lys Leu Asn Gln Leu Trp Glu  
50 55 60

Lys Ala Gln Arg Leu His Leu Pro Pro Val Arg Leu Ala Glu Leu His  
65 70 75 80

Ala Asp Leu Lys Ile Gln Glu Arg Asp Glu Leu Ala Trp Lys Lys Leu  
85 90 95

Lys Leu Asp Gly Leu Asp Glu Asp Gly Glu Lys Glu Ala Arg Leu Ile  
100 105 110

Arg Asn Leu Asn Val Ile Leu Ala Lys Tyr Gly Leu Asp Gly Lys Lys  
 115 120 125

Asp Ala Arg Gln Val Thr Ser Asn Ser Leu Ser Gly Thr Gln Glu Asp  
 130 135 140

Gly Leu Asp Asp Pro Arg Leu Glu Lys Leu Trp His Lys Ala Lys Thr  
 145 150 155 160

Ser Gly Lys Phe Ser Gly Glu Glu Leu Asp Lys Leu Trp Arg Glu Phe  
 165 170 175

Leu His His Lys Glu Lys Val His Glu Tyr Asn Val Leu Leu Glu Thr  
 180 185 190

Leu Ser Arg Thr Glu Glu Ile His Glu Asn Val Ile Ser Pro Ser Asp  
 195 200 205

Leu Ser Asp Ile Lys Gly Ser Val Leu His Ser Arg His Thr Glu Leu  
 210 215 220

Lys Glu Lys Leu Arg Ser Ile Asn Gln Gly Leu Asp Arg Leu Arg Arg  
 225 230 235 240

Val Ser His Gln Gly Tyr Ser Thr Glu Ala Glu Phe Glu Glu Pro Arg  
 245 250 255

Val Ile Asp Leu Trp Asp Leu Ala Gln Ser Ala Asn Leu Thr Asp Lys  
 260 265 270

Glu Leu Glu Ala Phe Arg Glu Glu Leu Lys His Phe Glu Ala Lys Ile  
 275 280 285

Glu Lys His Asn His Tyr Gln Lys Gln Leu Glu Ile Ala His Glu Lys  
 290 295 300

Leu Arg His Ala Glu Ser Val Gly Asp Gly Glu Arg Val Ser Arg Ser  
 305 310 315 320

Arg Glu Lys His Ala Leu Leu Glu Gly Arg Thr Lys Glu Leu Gly Tyr  
 325 330 335

Thr Val Lys Lys His Leu Gln Asp Leu Ser Gly Arg Ile Ser Arg Ala  
 340 345 350

Arg His Asn Glu Leu  
 355

<210> 22  
 <211> 378  
 <212> PRT  
 <213> Mus musculus

<400> 22

Met Gly Gly Pro Thr Arg Pro Ser Pro Val Ser Leu Leu Ala Leu Gln  
 1 5 10 15

Arg Lys Met Ala Pro Arg Arg Glu Arg Val Ser Thr Leu Pro Arg Leu  
 20 25 30

Gln Leu Leu Val Leu Leu Leu Leu Pro Leu Met Leu Val Pro Gln Pro  
 35 40 45

Ile Ala Gly His Gly Gly Lys Tyr Ser Arg Glu Lys Asn Glu Pro Glu  
 50 55 60

Met Ala Ala Lys Arg Glu Ser Gly Glu Glu Phe Arg Met Glu Lys Leu  
 65 70 75 80

Asn Gln Leu Trp Glu Lys Ala Lys Arg Leu His Leu Ser Pro Val Arg  
 85 90 95

Leu Ala Glu Leu His Ser Asp Leu Lys Ile Gln Glu Arg Asp Glu Leu  
 100 105 110

Asn Trp Lys Lys Leu Lys Val Glu Gly Leu Asp Lys Asp Gly Glu Lys  
 115 120 125

Glu Ala Lys Leu Ile His Asn Leu Asn Val Ile Leu Ala Arg Tyr Gly  
 130 135 140

Leu Asp Gly Arg Lys Asp Ala Gln Met Val His Ser Asn Ala Leu Asn  
 145 150 155 160

Glu Asp Thr Gln Asp Glu Leu Gly Asp Pro Arg Leu Glu Lys Leu Trp  
 165 170 175

His Lys Ala Lys Thr Ser Gly Lys Phe Ser Ser Glu Glu Leu Asp Lys  
 180 185 190

Leu Trp Arg Glu Phe Leu His Tyr Lys Glu Lys Ile Gln Glu Tyr Asn  
 195 200 205

Val Leu Leu Asp Thr Leu Ser Arg Ala Glu Glu Gly Tyr Glu Asn Leu  
 210 215 220



Leu Ser Pro Ser Asp Met Ala His Ile Lys Ser Asp Thr Leu Ile Ser  
225 230 235 240

Lys His Ser Glu Leu Lys Asp Arg Leu Arg Ser Ile Asn Gln Gly Leu  
245 250 255

Asp Arg Leu Arg Lys Val Ser His Gln Gly Tyr Gly Ser Thr Thr Glu  
260 265 270

Phe Glu Glu Pro Arg Val Ile Asp Leu Trp Asp Leu Ala Gln Ser Ala  
275 280 285

Asn Phe Thr Glu Lys Glu Leu Glu Ser Phe Arg Glu Glu Leu Lys His  
290 295 300

Phe Glu Ala Lys Ile Glu Lys His Asn His Tyr Gln Lys Gln Leu Glu  
305 310 315 320

Ile Ser His Gln Lys Leu Lys His Val Glu Ser Ile Gly Asp Pro Glu  
325 330 335

His Ile Ser Arg Asn Lys Glu Lys Tyr Val Leu Leu Glu Glu Lys Thr  
340 345 350

Lys Glu Leu Gly Tyr Lys Val Lys Lys His Leu Gln Asp Leu Ser Ser  
355 360 365

Arg Val Ser Arg Ala Arg His Asn Glu Leu  
370 375

<210> 23  
<211> 357  
<212> PRT  
<213> Rat

<400> 23

Leu Arg Asp Arg Val Ser Thr Leu Pro Arg Leu Gln Leu Leu Val Leu  
1 5 10 15

Leu Leu Leu Pro Leu Leu Leu Val Pro Gln Pro Ile Ala Gly His Gly  
20 25 30

Gly Lys Tyr Ser Arg Glu Lys Asn Glu Pro Glu Met Ala Ala Lys Arg  
35 40 45

Glu Ser Gly Glu Glu Phe Arg Met Glu Lys Leu Asn Gln Leu Trp Glu  
50 55 60

Lys Ala Lys Arg Leu His Leu Ser Pro Val Arg Leu Ala Glu Leu His  
 65 70 75 80

Ser Asp Leu Lys Ile Gln Glu Arg Asp Glu Leu Asn Trp Lys Lys Leu  
 85 90 95

Lys Val Glu Gly Leu Asp Gly Asp Gly Glu Lys Glu Ala Lys Leu Val  
 100 105 110

His Asn Leu Asn Val Ile Leu Ala Arg Tyr Gly Leu Asp Gly Arg Lys  
 115 120 125

Asp Thr Gln Thr Val His Ser Asn Ala Leu Asn Glu Asp Thr Gln Asp  
 130 135 140

Glu Leu Gly Asp Pro Arg Leu Glu Lys Leu Trp His Lys Ala Lys Thr  
 145 150 155 160

Ser Gly Lys Phe Ser Ser Glu Glu Leu Asp Lys Leu Trp Arg Glu Phe  
 165 170 175

Leu His Tyr Lys Glu Lys Ile His Glu Tyr Asn Val Leu Leu Asp Thr  
 180 185 190

Leu Ser Arg Ala Glu Glu Gly Tyr Glu Asn Leu Leu Ser Pro Ser Asp  
 195 200 205

Met Thr His Ile Lys Ser Asp Thr Leu Ala Ser Lys His Ser Glu Leu  
 210 215 220

Lys Asp Arg Leu Arg Ser Ile Asn Gln Gly Leu Asp Arg Leu Arg Lys  
 225 230 235 240

Val Ser His Gln Gly Tyr Gly Pro Ala Thr Glu Phe Glu Glu Pro Arg  
 245 250 255

Val Ile Asp Leu Trp Asp Leu Ala Gln Ser Ala Asn Phe Thr Glu Lys  
 260 265 270

Glu Leu Glu Ser Phe Arg Glu Glu Leu Lys His Phe Glu Ala Lys Ile  
 275 280 285

Glu Lys His Asn His Tyr Gln Lys Gln Leu Glu Ile Ser His Gln Lys  
 290 295 300

Leu Lys His Val Glu Ser Ile Gly Asp Pro Glu His Ile Ser Arg Asn  
 305 310 315 320

Lys Glu Lys Tyr Val Leu Leu Glu Glu Lys Thr Lys Glu Leu Gly Tyr  
325 330 335

Lys Val Lys Lys His Leu Gln Asp Leu Ser Ser Arg Val Ser Arg Ala  
340 345 350

Arg His Asn Glu Leu  
355

<210> 24  
<211> 348  
<212> PRT  
<213> Chicken

<400> 24

Met Gly Ala Thr Arg Thr Leu Val Ala Val Met Ala Ala Phe Leu Ala  
1 5 10 15

Val Ser Thr Arg Ala Ser Lys Tyr Thr Arg Glu Ala Asn Glu Gly Leu  
20 25 30

Ala Asp Ala Lys Arg Arg Glu Ala Gly Glu Phe Arg Val Val Arg Leu  
35 40 45

Asn Gln Val Trp Glu Lys Ala Gln Arg Leu Gln Leu Ser Ala Val Lys  
50 55 60

Leu Ala Glu Leu His Ser Asp Leu Lys Ile Gln Glu Lys Asp Glu Leu  
65 70 75 80

Ser Trp Lys Lys Leu Lys Ala Glu Gly Leu Gly Glu Asp Gly Glu Lys  
85 90 95

Glu Ala Lys Leu Arg Arg Asn Ile Asn Val Ile Met Thr Lys Tyr Gly  
100 105 110

Met Asn Gly Lys Lys Asp Ser His Leu Thr Asp Thr Asn Tyr Ile Lys  
115 120 125

Asp Gly Thr Glu Ser Asp Thr Leu Asp Asp Pro Arg Leu Glu Lys Leu  
130 135 140

Trp Ser Lys Ala Lys Thr Ser Gly Lys Phe Ser Asp Glu Glu Leu Asp  
145 150 155 160

Lys Leu Trp Arg Glu Phe Lys His His Lys Glu Lys Ile Arg Glu Tyr  
165 170 175

Asn Ile Leu Leu Glu Thr Val Ser Arg Thr Glu Asp Ile His Lys Lys  
180 185 190

Val Ile Asn Pro Ser Glu Glu Asn Pro Val Lys Glu Glu Val Leu His  
195 200 205

Asn Lys His Arg Glu Leu Lys Glu Lys Leu Arg Ser Ile Asn Gln Gly  
210 215 220

Phe Glu Arg Leu Arg Lys Val Ser His Gln Gly Tyr Asp Ala Thr Ser  
225 230 235 240

Glu Phe Glu Glu Pro Arg Val Ile Asp Leu Trp Asp Met Ala Lys Ser  
245 250 255

Ala Asn Phe Thr Glu Lys Glu Leu Glu Ser Phe Arg Glu Glu Leu Lys  
260 265 270

His Phe Glu Ala Lys Ile Glu Lys His His His Tyr Gln Lys Gln Leu  
275 280 285

Glu Ile Ser His Glu Lys Leu Lys His Ile Glu Gly Thr Gly Asp Lys  
290 295 300

Glu His Leu Asn Arg Asn Arg Glu Lys Tyr Ala Met Leu Glu Glu Lys  
305 310 315 320

Thr Lys Glu Leu Gly Tyr Lys Val Lys Lys His Leu Gln Asp Leu Ser  
325 330 335

Ser Arg Ile Ser Gln Gly Leu Gln His Asn Glu Leu  
340 345

<210> 25  
<211> 331  
<212> PRT  
<213> Zebrafish

<400> 25

Met Ala Gly Lys Tyr Ser Lys Glu Met Asn Glu Lys Asn Ala Ser Asp  
1 5 10 15

Lys Ser Asn Asn Gln Val Glu Phe Arg Ile Ala Lys Leu Asn Gln Val  
20 25 30

Trp Glu Lys Ala Ile Arg Met Gln Leu Ala Pro Val Arg Leu Ser Glu  
35 40 45

Leu His Ser Asp Leu Lys Ile Gln Glu Lys Asp Glu Leu Gln Trp Lys  
50 55 60

Lys Leu Lys Ala Glu Gly Met Asp Glu Asp Gly Glu Arg Glu Ala Lys  
65 70 75 80

Leu Arg Arg Asn Phe Asn Ile Ile Leu Ala Lys Tyr Gly Met Asp Gly  
85 90 95

Lys Lys Asp Thr Arg Thr Leu Asp Ser Asn Arg Leu Lys Asp His Glu  
100 105 110

Val Lys Ile Gly Asp Thr Phe Asp Asp Pro Lys Leu Asp Lys Leu Trp  
115 120 125

Asn Lys Ala Arg Thr Ser Gly Lys Phe Ser Asp Glu Glu Leu Gln Thr  
130 135 140

Leu His Arg Glu Phe Gln His His Lys Asp Lys Ile His Glu Tyr Asn  
145 150 155 160

Ile Val Met Asp Thr Val Ser Arg Thr Glu Glu Ile His Lys Asn Val  
165 170 175

Ile Ser Pro Leu Glu Gly Asp Val Lys Glu Asn Val Leu His Gln Lys  
180 185 190

His Thr Asp Leu Lys Gln Arg Met Arg Asp Leu Asn Gln Gly Phe Glu  
195 200 205

Arg Leu Arg Lys Ile Thr His Glu Gly Tyr Thr Asp Asp Ser Glu Phe  
210 215 220

Arg Glu Pro Arg Val Ile Glu Leu Trp Glu Met Ala Lys Arg Ser Asn  
225 230 235 240

Leu Ser Glu Asp Glu Leu Asp Ser Leu Lys Glu Glu Leu Arg His Phe  
245 250 255

Glu Thr Lys Val Glu Lys His Gln His Tyr Gln Glu Gln Leu Glu Leu  
260 265 270

Ser His Gln Lys Leu Lys His Val Glu Ala Leu Gly Asp Glu Asp His  
275 280 285

Ile Met Arg Asn Lys Glu Lys Tyr Asn Thr Leu Ala Glu Lys Ala Arg  
290 295 300

Glu Met Gly Tyr Lys Met Lys Lys His Leu Gln Asp Leu Thr Asn Lys  
 305 310 315 320

Leu Ser Lys Asn Gly Leu Gln His Asn Glu Leu  
 325 330

<210> 26  
 <211> 379  
 <212> PRT  
 <213> Fruit fly  
 <400> 26

Met Val Arg Ser Ala Leu Val Val Ala Ala Ile Ala Leu Ser Val Leu  
 1 5 10 15

Ile Ala Leu Gln Gly Val Asp Ala Asp Lys Lys Gln Ser Lys Lys Tyr  
 20 25 30

Ser Lys Glu Ala Asn Asp Pro His Phe Gln Gln Val Lys Gln Glu Lys  
 35 40 45

Tyr Asp Pro Asp Phe Lys Ser Ile Gln Arg Pro Phe Arg Met Ala Lys  
 50 55 60

Leu Asn Leu Val Trp Ala Lys Ala Gln Asn Arg Leu Thr Glu Pro Lys  
 65 70 75 80

Leu Lys Ser Leu Tyr Met Glu Leu Lys Ile His Asp Lys Glu Glu Ile  
 85 90 95

Ala Trp Lys Gln Leu Asn Ser Gln His Lys Asp Lys Asp Gly Leu Lys  
 100 105 110

Ala Asp Glu Leu Arg Arg Lys Leu Ile Gly Ile Met Ser Ser Tyr Asp  
 115 120 125

Leu Leu Glu His Phe Asp Asp Thr Gln Asp Thr Glu Lys Leu Lys Pro  
 130 135 140

Tyr Lys Lys Phe His Asp Ala Glu Glu Arg His Arg Asn Lys Ser Leu  
 145 150 155 160

Phe Lys Asp Lys Lys Leu Asn Arg Leu Trp Glu Lys Ala Glu Ile Ser  
 165 170 175

Gly Phe Thr Ala Glu Glu Leu Lys Ser Leu Lys Gln Glu Phe Asp His  
 180 185 190

His Gln Asp Lys Val Asp Val Tyr Tyr Ser Leu Leu Glu Asn Ile Gly  
195 200 205

Thr Val Asp Thr Asp Lys His Glu Asn Ala Ile Asn Thr Glu Asp Leu  
210 215 220

Asp Thr Tyr Asn Leu Ile Ser Asn Asp Val Asn Glu Asn Asp Ile Lys  
225 230 235 240

Thr His Ala Gln Asn Val Lys Ser Phe Glu Asn Asp Leu Asn Thr Leu  
245 250 255

Arg Gly His His Thr Gly Ile Lys Asp His Tyr Asp Arg Leu Glu Arg  
260 265 270

Leu Val Ser Ser Gly Pro His Ser Gln Asp Phe Ile Glu Pro Lys Val  
275 280 285

Gln Gly Leu Trp Arg Val Ala Gln Ala Ser Asn Phe Thr Val Lys Glu  
290 295 300

Leu Glu Ser Ile Lys Thr Glu Leu His His Phe Glu Ser Arg Leu Leu  
305 310 315 320

Lys Leu Arg His Leu His Ala Glu His Ala Leu Gln Lys Glu Lys Tyr  
325 330 335

Lys Gly Glu Lys Val Lys Asp Lys Ser Ser Arg Phe Glu Glu Met Glu  
340 345 350

Asp Gln Leu Lys Lys Gln Thr Arg Lys Val Glu Lys Leu Gln Glu Asn  
355 360 365

Ile Glu Lys Thr Ile Phe Lys His Thr Glu Leu  
370 375

<210> 27  
<211> 400  
<212> PRT  
<213> Mosquito

<400> 27

Glu Leu Cys Pro Ile Ala Arg Arg Lys Arg Gly Ile Lys His Thr Leu  
1 5 10 15

Thr Met Pro Leu Phe Thr Arg Leu Cys Val Ile Val Phe Thr Val Leu  
20 25 30

Val Cys Asn His Val Val Gln Ser Glu Lys Ala His Ser Lys Tyr Ser  
35 40 45  
Lys His Ala Asn Ala Leu Pro Asp Ser Glu Ile Tyr Glu Pro Asp Phe  
50 55 60  
Arg Asn Ile Gln Arg Pro Phe Arg Met Ala Lys Leu Asn Leu Val Trp  
65 70 75 80  
Thr Lys Ala Gln His Arg Leu Thr Glu Pro Lys Leu Lys Ser Leu Tyr  
85 90 95  
Thr Glu Leu Lys Leu His Asp Lys Glu Glu Leu Thr Tyr Lys Gln Leu  
100 105 110  
Lys Glu Lys Asp Lys Asp Gly Leu Lys Glu Ala Glu Leu Arg Asn Lys  
115 120 125  
Leu Val Ser Ile Met Ser Thr Tyr Gly Leu Leu Glu His Phe Asp Asp  
130 135 140  
Thr Gln Asp Pro Glu Lys Tyr Lys Leu Ala Lys Ser Ser Asp Gly Ala  
145 150 155 160  
Pro Lys Lys Asp Thr Tyr Lys Asn Lys Ser Leu Phe Lys Asp Lys Lys  
165 170 175  
Leu Asn Lys Leu Trp Asp Lys Ala Glu Ser Ala Gly Phe Thr Lys Glu  
180 185 190  
Glu Leu Asp Ala Leu Arg Glu Glu Phe Asp His His Gln Ala Lys Ile  
195 200 205  
Asp Val Tyr Tyr Ser Leu Leu Glu Arg Leu Gly Asp Asp Asp Asp Gly  
210 215 220  
Gly Ala Ala Gly Gln Gly Ser Arg Arg Asp Asp Asp Ala Leu Leu Asn  
225 230 235 240  
Ala Val Asn Asp Glu Glu His Asp Arg Tyr Asn Glu Val Asp Arg Ala  
245 250 255  
Glu Glu Thr Asp Arg Ser Gln Pro Gly Ala Asn Lys Gln His Ala Tyr  
260 265 270  
Leu His Lys Ser Asn Gln Leu Arg Glu Lys His Arg Glu Ile Arg Asp  
275 280 285



Asn Phe Asp Arg Leu Asp Arg Ile Ala Ser Lys Gly Pro Lys Ser Gln  
 290 295 300

Asp Phe Val Glu Pro Lys Val Gln Gly Leu Trp Arg Val Ala Leu Ala  
 305 310 315 320

Ser Asp Phe Ser Ala Asp Glu Leu Ala Ser Leu Lys Val Glu Leu Leu  
 325 330 335

His Tyr Glu Ser Arg Leu Leu Lys Leu Arg His Met His Ala Glu His  
 340 345 350

Ala Leu Ser Leu Glu Lys His Lys His Ser Asp Ala Lys Ala Asp Thr  
 355 360 365

His Lys Leu Met Glu Asp Asn Ile Lys Lys Gln Thr Arg Lys Val Glu  
 370 375 380

Lys Met Gln Glu Glu Val Glu Arg Arg Ile Phe Lys His Ser Glu Leu  
 385 390 395 400

<210> 28  
 <211> 331  
 <212> PRT  
 <213> Flatworm

<400> 28

Met Arg Asn His Phe Ser Phe Leu Leu Phe Leu Leu Val Ile Gly Ser  
 1 5 10 15

Ala His Asn Lys Lys Thr Gln Tyr Arg Thr Glu Arg Ile Asn Phe Ile  
 20 25 30

Tyr Glu Lys Ala Leu Gln His Val Thr Asp Arg Gln Asn Leu Ala Arg  
 35 40 45

Leu Glu Lys Glu Leu Ser Gly Tyr Asp Ala Ile Tyr Leu Ala Ser Lys  
 50 55 60

Ser Asn Arg Gln Gly Thr Gln Gly Thr Lys Glu Ile Asp Lys Ile Asp  
 65 70 75 80

Asp Lys Leu Gly Lys Ile Leu Glu Lys Tyr Gly Leu Glu Lys Ala Val  
 85 90 95

Leu Ala Phe Lys Glu Lys Tyr Lys His Lys Asn Leu Phe Gln Gln Thr  
 100 105 110

Asp Asp Asn Glu Pro Leu Pro Ser Gly Lys Phe Thr Asp Gln Asn Leu  
115 120 125

Gln Lys Leu Trp Ser Gln Ala Gln Asn Gly Lys Phe Ser Gln Lys Glu  
130 135 140

Leu Asn Ala Leu His Gly Glu Leu Lys Glu Val Glu Gln Lys Met Arg  
145 150 155 160

Val Tyr Glu Asp Gln Leu Asp Asp Phe Lys Lys Val Pro His Glu Asn  
165 170 175

Ser Ile Gln His Asp Ile Glu Ser Ile Gly Asp Lys Thr Lys Lys Leu  
180 185 190

Lys Ala Ala Asn Arg Glu Leu Asn Asp His Leu Asp Glu Val His Arg  
195 200 205

Lys Val Thr Ser Glu Glu Phe Ser Pro Phe Asn Glu Pro Arg Val Lys  
210 215 220

Arg Leu Trp Lys Leu Ala Gln Glu Asn Glu Lys Leu Thr Pro His Glu  
225 230 235 240

Leu Ser Val Leu Lys Asp Glu Leu Ser His Phe Glu Ser Gln Leu Lys  
245 250 255

Lys Ile Glu Phe His Lys Val Phe Phe Phe Val Ala Asn Ser Cys Pro  
260 265 270

Lys Arg Gly Lys Asn Glu Glu Val Ser Arg Leu Gln Glu Asp Ala Glu  
275 280 285

Glu Arg Gly Lys Asp Lys Ser Gln Val Tyr Glu Asn Leu Glu Leu Ser  
290 295 300

Ile Lys His Glu Lys Leu Asn Arg Lys Ala Arg Lys Leu Glu Lys Tyr  
305 310 315 320

Ile Glu Glu Lys Ile Ile Ile His Arg Glu Leu  
325 330

<210> 29  
<211> 6  
<212> PRT  
<213> Artificial sequence  
  
<220>  
<223> Synthetic peptide

<400> 29

Ala Glu Ala Glu Thr Gly  
1 5